

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/564,585
Source: IFWP
Date Processed by STIC: 1/30/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/30/2006

PATENT APPLICATION: US/10/564,585

TIME: 14:59:12

Input Set : A:\61835-3 SEQ LIST.txt

Output Set: N:\CRF4\01302006\J564585.raw

3 <110> APPLICANT: Vanaja, Donkena Krishna
 4 Young, Charles Y.F.
 6 <120> TITLE OF INVENTION: Methods And Compositions For Diagnosis, Staging and
 Prognosis of
 7 Prostate Cancer
 9 <130> FILE REFERENCE: 61835-3
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/564,585
 C--> 11 <141> CURRENT FILING DATE: 2006-01-13
 11 <150> PRIOR APPLICATION NUMBER: US 60/487,553
 12 <151> PRIOR FILING DATE: 2003-07-14
 14 <150> PRIOR APPLICATION NUMBER: PCT/US2004/022850
 15 <151> PRIOR FILING DATE: 2004-07-14
 17 <160> NUMBER OF SEQ ID NOS: 52
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 3614
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (41)..(1399)
 31 <400> SEQUENCE: 1
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 33 Met Gln Arg Gln Ala
 34 1 5
 36 ccc tac aat atc agg cgc agc tct aca tca ggg gac acc gag gag gag 103
 37 Pro Tyr Asn Ile Arg Arg Ser Ser Thr Ser Gly Asp Thr Glu Glu Glu
 38 10 15 20
 40 gag gag gag gag gtg gtg cca ttc tcc tca gat gaa cag aaa cgg agg 151
 41 Glu Glu Glu Glu Val Val Pro Phe Ser Ser Asp Glu Gln Lys Arg Arg
 42 25 30 35
 44 tca gag gct gca agc ggt gtt ctg agg agg aca gct ccc cgg gag cac 199
 45 Ser Glu Ala Ala Ser Gly Val Leu Arg Arg Thr Ala Pro Arg Glu His
 46 40 45 50
 48 tcc tac gtc ctg tca gcg gcc aag aag agc act ggc agt cct acc cag 247
 49 Ser Tyr Val Leu Ser Ala Ala Lys Lys Ser Thr Gly Ser Pro Thr Gln
 50 55 60 65
 52 gag aca cag gca ccg ttt atc gcg aag agg gtg gag gtg gtg gaa gag 295
 53 Glu Thr Gln Ala Pro Phe Ile Ala Lys Arg Val Glu Val Val Glu Glu
 54 70 75 80 85
 56 gac ggg cct tct gag aag agc cag gac cca cct gct ctg gca aga tcc 343
 57 Asp Gly Pro Ser Glu Lys Ser Gln Asp Pro Pro Ala Leu Ala Arg Ser
 58 90 95 100
 60 act cct ggc tca aac agc tca aga ggt gag gaa att gtc cgc ctg cag 391

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62				105					110				115				
64	atc	ctg	aca	ccc	agg	gca	gga	ctc	cgc	ctg	gtg	gcc	cca	gac	gtg	gaa	439
65	Ile	Leu	Thr	Pro	Arg	Ala	Gly	Leu	Arg	Leu	Val	Ala	Pro	Asp	Val	Glu	
66			120					125					130				
68	ggc	atg	agc	tcc	agt	gcc	act	tca	gtc	tct	gct	gtc	cct	gct	gat	agg	487
69	Gly	Met	Ser	Ser	Ser	Ala	Thr	Ser	Val	Ser	Ala	Val	Pro	Ala	Asp	Arg	
70		135					140					145					
72	aag	agc	aac	agc	aca	gca	gcc	cag	gag	gat	gca	aag	gca	gac	cca	aag	535
73	Lys	Ser	Asn	Ser	Thr	Ala	Ala	Gln	Glu	Asp	Ala	Lys	Ala	Asp	Pro	Lys	
74	150					155				160						165	
76	ggg	gcc	ttg	gct	gat	tgt	gag	ggg	aag	gat	gta	ccc	acc	agg	gtc	gga	583
77	Gly	Ala	Leu	Ala	Asp	Cys	Glu	Gly	Lys	Asp	Val	Pro	Thr	Arg	Val	Gly	
78				170					175						180		
80	gag	gcc	tgg	cag	gag	agg	cct	gga	gct	cca	aga	ggg	ggc	caa	gga	gac	631
81	Glu	Ala	Trp	Gln	Glu	Arg	Pro	Gly	Ala	Pro	Arg	Gly	Gly	Gln	Gly	Asp	
82			185						190					195			
84	cca	gct	gta	ccc	gct	cag	caa	cct	gca	gat	ccc	agc	acc	cca	gag	cgg	679
85	Pro	Ala	Val	Pro	Ala	Gln	Gln	Pro	Ala	Asp	Pro	Ser	Thr	Pro	Glu	Arg	
86		200						205					210				
88	cag	agc	agc	ccc	agc	gga	tct	gag	caa	ctt	gtc	aga	cga	gag	agt	tgt	727
89	Gln	Ser	Ser	Pro	Ser	Gly	Ser	Glu	Gln	Leu	Val	Arg	Arg	Glu	Ser	Cys	
90		215					220					225					
92	ggc	agt	agc	gtg	ttg	act	gat	ttt	gag	ggg	aag	gat	gtg	gcc	acc	aag	775
93	Gly	Ser	Ser	Val	Leu	Thr	Asp	Phe	Glu	Gly	Lys	Asp	Val	Ala	Thr	Lys	
94	230					235					240					245	
96	gtc	gga	gag	gcc	tgg	cag	gac	agg	cct	aga	gcc	cca	aga	ggg	ggc	caa	823
97	Val	Gly	Glu	Ala	Trp	Gln	Asp	Arg	Pro	Arg	Ala	Pro	Arg	Gly	Gly	Gln	
98				250					255					260			
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101	Gly	Asp	Pro	Ala	Val	Pro	Thr	Gln	Gln	Pro	Ala	Asp	Pro	Ser	Thr	Pro	
102				265					270					275			
104	gaa	cag	cag	aac	agc	ccc	agc	gga	tct	gag	caa	ttc	gtc	aga	cga	gag	919
105	Glu	Gln	Gln	Asn	Ser	Pro	Ser	Gly	Ser	Glu	Gln	Phe	Val	Arg	Arg	Glu	
106			280						285				290				
108	agc	tgc	acc	agc	agg	gtg	agg	agc	ccc	tcg	agc	tgc	atg	gtc	act	gtt	967
109	Ser	Cys	Thr	Ser	Arg	Val	Arg	Ser	Pro	Ser	Ser	Cys	Met	Val	Thr	Val	
110		295					300					305					
112	act	gtc	act	gcc	aca	tct	gag	cag	cct	cac	att	tat	att	cca	gcc	ccc	1015
113	Thr	Val	Thr	Ala	Thr	Ser	Glu	Gln	Pro	His	Ile	Tyr	Ile	Pro	Ala	Pro	
114	310					315					320					325	
116	gca	agt	gaa	ttg	gac	tcc	agc	tct	acc	acc	aaa	ggg	att	ctc	ttc	gtg	1063
117	Ala	Ser	Glu	Leu	Asp	Ser	Ser	Ser	Thr	Thr	Lys	Gly	Ile	Leu	Phe	Val	
118				330					335				340				
120	aag	gag	tac	gtg	aat	gct	agt	gaa	gtg	tct	tct	ggg	aag	cca	gta	tct	1111
121	Lys	Glu	Tyr	Val	Asn	Ala	Ser	Glu	Val	Ser	Ser	Gly	Lys	Pro	Val	Ser	
122				345					350				355				
124	gca	cgc	tat	agc	aac	gtc	agc	agc	att	gag	gac	tca	ttc	gcc	atg	gag	1159
125	Ala	Arg	Tyr	Ser	Asn	Val	Ser	Ser	Ile	Glu	Asp	Ser	Phe	Ala	Met	Glu	

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126	360	365	370	
128	aag aag cct cca tgt ggc agc act cca tac tct gag agg aca act gga	1207		
129	Lys Lys Pro Pro Cys Gly Ser Thr Pro Tyr Ser Glu Arg Thr Thr Gly			
130	375 380 385			
132	ggg atc tgt act tac tgc aac cgt gag atc cga gac tgt cca aag att	1255		
133	Gly Ile Cys Thr Tyr Cys Asn Arg Glu Ile Arg Asp Cys Pro Lys Ile			
134	390 395 400 405			
136	acc cta gaa cat ctt ggt atc tgc tgc cat gaa tat tgc ttt aag tgt	1303		
137	Thr Leu Glu His Leu Gly Ile Cys Cys His Glu Tyr Cys Phe Lys Cys			
138	410 415 420			
140	ggg att tgc agt aaa ccg atg ggc gat ctc ctg gat cag atc ttc att	1351		
141	Gly Ile Cys Ser Lys Pro Met Gly Asp Leu Leu Asp Gln Ile Phe Ile			
142	425 430 435			
144	cac cgt gac acc att cac tgt ggg aaa tgc tat gag aag ctc ttc tag	1399		
145	His Arg Asp Thr Ile His Cys Gly Lys Cys Tyr Glu Lys Leu Phe			
146	440 445 450			
148	cgacccccca ccgccaggct gatcagaagc tgatgactcg tggacaaaatt tggctgtccc	1459		
150	cagttttgcc ccaagttgct gtctccccct cctcacctc ctccctccct gtttgatttc	1519		
152	ttcatgcttt tgcccttctc aagttgaagt tgcatacatc caatatcgta tcttaatgat	1579		
154	gctatgataa ttgcttggt gtgtagcttc ttgtagctta gaaagcgctt tatgccccatg	1639		
156	atgtcatttc aggtcaacc aaagaggatc aaacaggaat tccatcttgg cttccctaag	1699		
158	acagattggc tttctaataa gtttaagtgg gcagaagtgt agggttcagt gtgtcctgac	1759		
160	tcccttgagg cttataatgg gccaaagtga agactgttga tgatccctgg tgggtaaatt	1819		
162	gcagacatca aatgctaggg attggcatag gctagtgttt agcttgctta tttgccatat	1879		
164	ctattttttt aaatttccat acacttgtaa aagtagttag ttgcttttga ttgagttata	1939		
166	tagcagtttt tcatttggtc ttccactcac cgttcactat atttgagtgt tcccttacag	1999		
168	gtatgttggc atgtgttggg aaatttacac aattaggttt aaattcagta ggatgtgatt	2059		
170	ttgggggtgg actgatcaaa gtgatatctg tgtctgttgg aatcttgata gctgattaat	2119		
172	ttgccctcaa ttctgctccc tgaacttcac acataaatct tcccaagtgg gttttagggt	2179		
174	gtatagatcc cagcaggatt aaggaagtgg aaaagcagct aacatttctt gaggtcttac	2239		
176	cacatagcag gcactgtcac agagtaatgg cattaatccc cataataatc ctgtgaagg	2299		
178	gatattctca tcccatctta gacatgagga tattggaact cagagagggt gctattgcat	2359		
180	tgcgcagaac gctacagagc ccatgctctt cccagagcag caccacaaaa agcaagcatt	2419		
182	gattttgtgc tcagtgtgtg ccaagcactg tgcagagggt acacagttcc tgccaggtta	2479		
184	acaccctccc ttcaggcctc ccaaaggcat aggcttgcaa agagcagaag gtgtgaaatc	2539		
186	acactcttcc tctgggcatc ctggatccct gaattatccc ccccccatg aagtacttca	2599		
188	agggccaaagc tgccccttcc cctcctctcc gcccatgaaa atgcctccaa actgagatgc	2659		
190	tttcagctga gaacagattt gactcacaga cattacaaaa gaggagcttg tgaatccagg	2719		
192	aaaagctcca gggggctagc tgatctgagc agagagcttt cagtgaacca ttttcctgtc	2779		
194	tagactctgc cttaaagctag tggcaactgc tggggcccca ggtacttggg acatggaaac	2839		
196	tcggtggatg gctgggcaga tgtaagcctg tccatgcagt cagccgatcc tctgtcagg	2899		
198	ttcagctgga ctctgccatc tgtgggcccc gcactactct gtaagttcct tgaaaggaa	2959		
200	aacaacctta gagtatttct gatacaaaat gagggcctct gctcttgatt taattataaa	3019		
202	atgtctacgt ctttctccag tttctgagcc ctatgcacat tggcttgtgg gcttgttctt	3079		
204	cctgccaaat gatcagagag ggaacattcc atttatttgt agtggatttc ctctggagg	3139		
206	catgtacca cactaaatac caactgctct tcctcagctg tagtcccaa catcagactt	3199		
208	ggcacgtggg ggacactaac acacaggcac tcaatgaatg agtgaaggaa ataaaagtca	3259		
210	cccccgctt gtgagaagg gtctatcccc ctgagtcctc agtgcaggac cagtggatga	3319		
212	aaggcaagg aaagaggccc aagataggct ggcttcccc gttcaaggta tagtctgcct	3379		

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214 ttaaggggagt tttagaacca acatgcaaga cattgaaaga aatcttgcaa gagccattat 3439
216 tgacttagat ccaaaacagc ctctctcatg tctaaaaagg cacagaattt tgcagatctg 3499
218 aggaagaggg atgcattacc tttttgcttc ttttcaattg cttagtgttt ctaatcatac 3559
220 ttaatccaca ctaatgtgcg caattataat aaatgctaaa atatcaaaaa aaaaa 3614
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224 <211> LENGTH: 452
225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
228 <400> SEQUENCE: 2
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234 Asp Thr Glu Glu Glu Glu Glu Glu Glu Val Val Pro Phe Ser Ser Asp
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238 Glu Gln Lys Arg Arg Ser Glu Ala Ala Ser Gly Val Leu Arg Arg Thr
239 35 40 45
242 Ala Pro Arg Glu His Ser Tyr Val Leu Ser Ala Ala Lys Lys Ser Thr
243 50 55 60
246 Gly Ser Pro Thr Gln Glu Thr Gln Ala Pro Phe Ile Ala Lys Arg Val
247 65 70 75 80
250 Glu Val Val Glu Glu Asp Gly Pro Ser Glu Lys Ser Gln Asp Pro Pro
251 85 90 95
254 Ala Leu Ala Arg Ser Thr Pro Gly Ser Asn Ser Ser Arg Gly Glu Glu
255 100 105 110
258 Ile Val Arg Leu Gln Ile Leu Thr Pro Arg Ala Gly Leu Arg Leu Val
259 115 120 125
262 Ala Pro Asp Val Glu Gly Met Ser Ser Ser Ala Thr Ser Val Ser Ala
263 130 135 140
266 Val Pro Ala Asp Arg Lys Ser Asn Ser Thr Ala Ala Gln Glu Asp Ala
267 145 150 155 160
270 Lys Ala Asp Pro Lys Gly Ala Leu Ala Asp Cys Glu Gly Lys Asp Val
271 165 170 175
274 Pro Thr Arg Val Gly Glu Ala Trp Gln Glu Arg Pro Gly Ala Pro Arg
275 180 185 190
278 Gly Gly Gln Gly Asp Pro Ala Val Pro Ala Gln Gln Pro Ala Asp Pro
279 195 200 205
282 Ser Thr Pro Glu Arg Gln Ser Ser Pro Ser Gly Ser Glu Gln Leu Val
283 210 215 220
286 Arg Arg Glu Ser Cys Gly Ser Ser Val Leu Thr Asp Phe Glu Gly Lys
287 225 230 235 240
290 Asp Val Ala Thr Lys Val Gly Glu Ala Trp Gln Asp Arg Pro Arg Ala
291 245 250 255
294 Pro Arg Gly Gly Gln Gly Asp Pro Ala Val Pro Thr Gln Gln Pro Ala
295 260 265 270
298 Asp Pro Ser Thr Pro Glu Gln Gln Asn Ser Pro Ser Gly Ser Glu Gln
299 275 280 285
302 Phe Val Arg Arg Glu Ser Cys Thr Ser Arg Val Arg Ser Pro Ser Ser
303 290 295 300
306 Cys Met Val Thr Val Thr Val Thr Ala Thr Ser Glu Gln Pro His Ile
307 305 310 315 320

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310 Tyr Ile Pro Ala Pro Ala Ser Glu Leu Asp Ser Ser Ser Thr Thr Lys
311                               325                               330                               335
314 Gly Ile Leu Phe Val Lys Glu Tyr Val Asn Ala Ser Glu Val Ser Ser
315                               340                               345                               350
318 Gly Lys Pro Val Ser Ala Arg Tyr Ser Asn Val Ser Ser Ile Glu Asp
319                               355                               360                               365
322 Ser Phe Ala Met Glu Lys Lys Pro Pro Cys Gly Ser Thr Pro Tyr Ser
323                               370                               375                               380
326 Glu Arg Thr Thr Gly Gly Ile Cys Thr Tyr Cys Asn Arg Glu Ile Arg
327 385                               390                               395                               400
330 Asp Cys Pro Lys Ile Thr Leu Glu His Leu Gly Ile Cys Cys His Glu
331                               405                               410                               415
334 Tyr Cys Phe Lys Cys Gly Ile Cys Ser Lys Pro Met Gly Asp Leu Leu
335                               420                               425                               430
338 Asp Gln Ile Phe Ile His Arg Asp Thr Ile His Cys Gly Lys Cys Tyr
339                               435                               440                               445
342 Glu Lys Leu Phe
343                               450
346 <210> SEQ ID NO: 3
347 <211> LENGTH: 23
348 <212> TYPE: DNA
349 <213> ORGANISM: artificial sequence
351 <220> FEATURE:
352 <223> OTHER INFORMATION: ZNF 185 forward primer
354 <400> SEQUENCE: 3
355 tggatgaaag gcaaggtaaa gag                                     23
358 <210> SEQ ID NO: 4
359 <211> LENGTH: 26
360 <212> TYPE: DNA
361 <213> ORGANISM: artificial sequence
363 <220> FEATURE:
364 <223> OTHER INFORMATION: ZNF 185 reverse primer
366 <400> SEQUENCE: 4
367 ttctaaaact cccttaaagg cagact                                     26
370 <210> SEQ ID NO: 5
371 <211> LENGTH: 23
372 <212> TYPE: DNA
373 <213> ORGANISM: artificial sequence
375 <220> FEATURE:
376 <223> OTHER INFORMATION: ZNF 185 probe
378 <400> SEQUENCE: 5
379 ccaagatagg ctggcttccc ccg                                     23
382 <210> SEQ ID NO: 6
383 <211> LENGTH: 30
384 <212> TYPE: DNA
385 <213> ORGANISM: artificial sequence
387 <220> FEATURE:
388 <223> OTHER INFORMATION: PSP94 forward primer
390 <400> SEQUENCE: 6

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; N Pos. 505

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:480